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HUSBANDRY PRACTICES:  
THE WAY FORWARD**

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## MODERN ANIMAL BREEDING TECHNIQUES FOR DEVELOPING COUNTRIES

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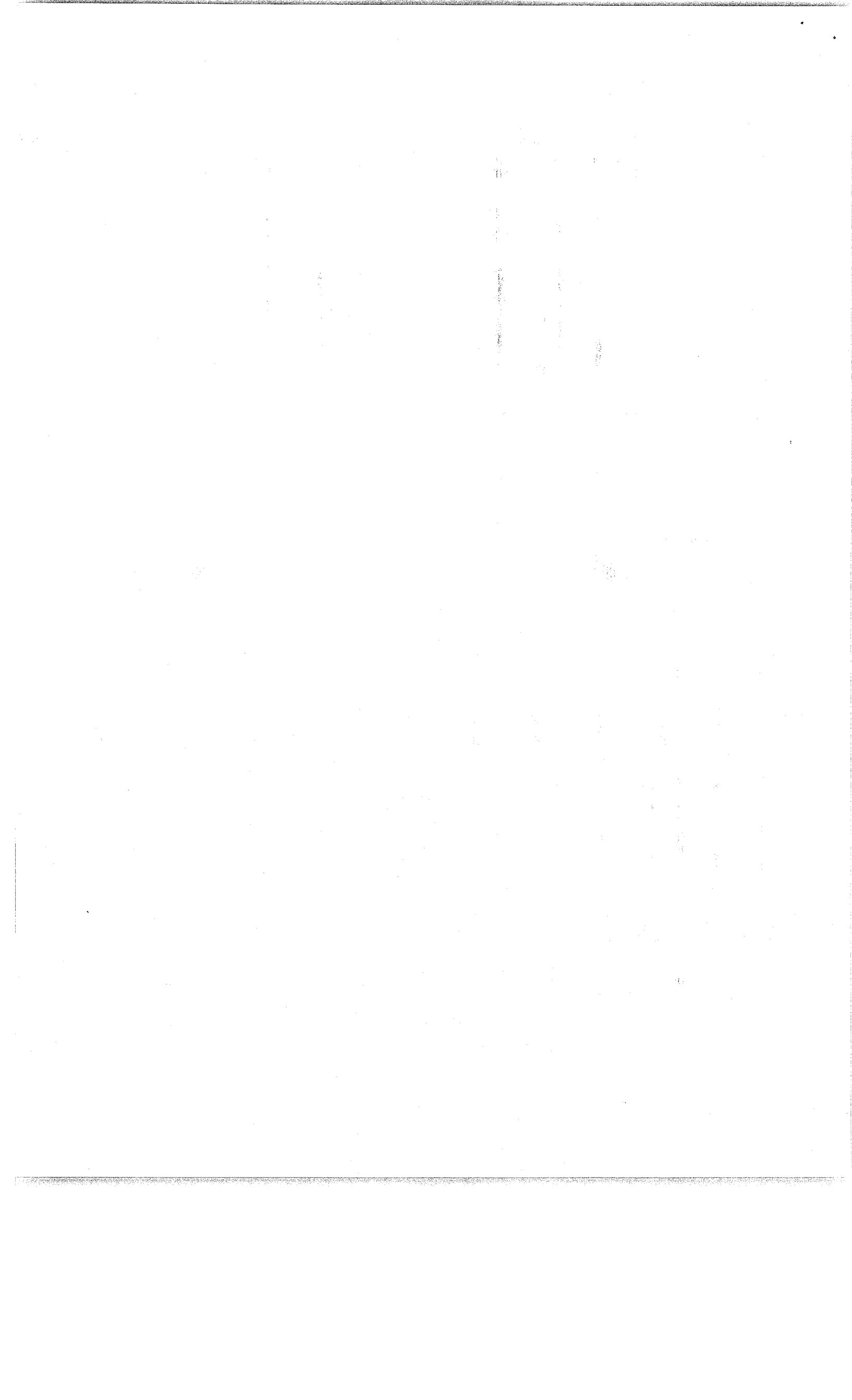
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In late 1990, L. Dale Van Vleck has pointed out the impact of research on the livestock improvement done by quantitative geneticist and molecular biology. He mentioned that the history of molecular biology began when the Watson - Crick Model for genetic material around 50 years ago (1). They had worked out, rather amazingly, the structure and coding pattern for DNA. Enthusiasts, no doubt, thought that all genetic mysteries would soon be solved. However, quantitative animal breeders were naturally skeptical. Who would have predicted that the gene for making bovine growth hormone (bGH) could be cut out of the chromosome of a cow and inserted into bacteria which then manufactures rather cheaply so much bGH that perhaps 20% fewer dairy cows will be needed? Who would have thought that the DNA structure of an entire chromosome might be sequenced? Who would have thought a gene from a man can be added to the genome of a mouse, or a pig or a sheep to create what are called transgenic. That much of chromosome seems to contain non-essential information? That some genes are repeated in the same and different chromosome? That a couple of missing base pairs are implicated in cystic fibrosis? That chromosome can be biologically sliced at predictable break point and then sorted by size – the restriction fragment length polymorphism? Quantitative geneticist, however quickly recover after acknowledging the impossible and ask the skeptic's question: what, of all that has been learned from molecular biology, can be applied to livestock improvement? At present, and after more than 50 years of exciting and amazing discovery, the answer seems to be not much. If anything, from molecular can be applied to animal improvement.

For livestock improvement, the greatest success story from biotechnology has been artificial insemination (AI). Although most of the successes of AI have been with dairy cattle, a great potential exist for most species. Modern history of AI is only a little more than 60 years old. Unquestionably, scientific knowledge gained from development of AI has increased in that time period but that knowledge is modest compared to that from molecular biology. The coming together, however, of the reproductive technology of AI, the electronic technology of computer combined with long established unbiased prediction procedures for genetic evaluation are responsible for significant genetic improvement in dairy cattle, particularly in the last 20-25 years. The potential exist for other species. The history of AI is relatively little gain in knowledge but relatively large gains when applied. Nevertheless, that history is instructive. What is distinctive is how the quantitative sciences, computing and statistic have complemented the biological science of reproductive biology. That same interaction should be the theme for cooperation between molecular and quantitative geneticist. The two poles of genetics really are synergistic and should not be antagonistic.

Natural selection seems to lead to an optimally balanced animal. Balance often is some intermediate between extremes that considers all characteristics. Change due to natural selection is slow. Artificial selection generally is toward an extreme; often one or a few traits. If change due to selection is slow, as is usual with



methods of quantitative genetics, then a little indirect selection is often sufficient to retain a reasonably well-balanced animal. On the other hand, change due to molecular geneticist, such as adding Booroola gene to a breed, can be rapid. In such case, will having lots of twins and triplets be advantage if maternal characteristics of the ewe are still at an optimum for rearing singles? The whole animal needs to be considered if "major" genes are inserted in to the genome of a population.

Transgenic animal is another way has proved very valuable but not permanently changing the gene of farm animal. Growth hormone is perhaps the best-known example to livestock producer of a successful transgenic. The gene, however, was not moved from another animal to the cow but was moved from the cow to bacteria, which then became the workers in a factory from production, i.e., the growth hormone from outside sources becomes an environmental factor influencing production of the cow. The genotype of the cow has not been changed. The superior performance cannot be transmitted from parent to progeny.

The most significant research progress occurred in the estimation of genetic parameters. This fast development is affected by the development of quantitative genetic models, especially after the launching of DFREML, REML, VCE and PEST software's. Best Linier Unbiased Prediction (BLUP). For the latest development this methods can also be used of estimate additive and non additive variances of body weight, egg weight and egg production for quails with an animal model analysis (2).

This method has been applied in Center for Bali cattle Improvement Project. The data of weaning weight, yearling and post weaning daily gains registered from 1983 to 2000 were utilized. VCE4 an PEST (3) were used to estimate (co)variance and breeding values, respectively. The estimated heritability values were  $0.23 \pm 0.22$ ,  $0.38 \pm 0.02$  and  $0.27 \pm 0.02$  for weaning weight, yearling weight and post weaning daily gain respectively. Genetic correlation between weaning weight and post weaning daily gain, weaning weight and yearling weight and between post weaning daily gains and yearling weight were  $0.27 \pm 0.06$ ,  $0.72 \pm 0.03$  and  $0.86 \pm 0.02$ , respectively. Inbreeding coefficients average was 0.23 with maximum of 0.25 values. These result shows that the estimated breeding values in the breeding centre were higher than in all unit in base populations. However, the genetic trends of weaning weight and yearling weight showed a negative slope, while the genetic trend of post weaning daily gain showed a positive slope. These results also show that the genetic trends of all traits in Bali cattle were inconsistent, but the consistency can be increased in selection accurately done (4).

In dairy cattle monthly records can also be used to estimate the breeding value for milk yield and genetic parameter of some reproduction traits by using REML and BLUP methods. The data of milk and reproduction records for first, second and third lactations of FH cows calving in Taurus Dairy Farm from 1989 – 2002 were used. Total monthly records were 10.123, reproduction records consisted of 722 calving interval, 971 days open and 65 service per conception. The results show that heritability of milk yield based on single monthly record was higher at the middle lactation than those at the beginning and end months of lactation. The best single monthly record to estimated breeding values at the first lactation are 4<sup>th</sup> and 5<sup>th</sup> month, at the second and third lactation is 5<sup>th</sup> month record. The estimate of heritability value and the accuracy of estimated breeding value of cumulative production increase in the stage of lactation. The heritability of calving interval, days open and service per conception were low, genetic correlation of these traits with milk yield were high and their phenotypic correlation were low. So, single and cumulative monthly records can be used to estimate breeding value (5)

Test-day record has been used as selection criteria to evaluate the genetic values of dairy cattle, because the 305 days record is considered not practical, especially in most of developing countries. In order to get the best model, the data of milk production at first and second lactation from 1989-2000 at PT. Taurus Dairy Farms, Sukabumi were utilized. A total of 7503 test days records and 769 records of 305 days milk production originated from 456 cows, 40 sires and 342 dams were used. The model used were (1) Cumulative Model (CM) to analyze 305 days record, (2) Three models of Fixed Regression Test Days Model (FRTDM) and two models of Multiple Traits (MMT) to analyze test-day record. All seven models set year-season and year-lactation as fixed effects. The variance components were estimated using Animal Model by using REML and breeding values by using BLUP. The results indicate that the estimated heritability value for CM for model 1 is 0.308 and for model 2 is 0.314; for FRTDM: model 3 is 0.140, model 4 is 0.156 and model 5 is 0.095 and MMT: model 6 is 0.087-0.271 and for model 7 is 0.053-0.358. The Spearman correlation of breeding values among CM, FRTDM and MMT for all animals is 0.87-0.99 and for the sire is 0.83-0.98. From this analysis it can be concluded that the FRTDM is a flexible, accurate and efficient model for evaluating the genetic value of dairy cattle (6).

Single regression (SR), multiple regression (MR), and factor analysis (FA) methods for projecting lactation milk yield from part-lactation test-day records at regular 15-, 30-, and 45-day intervals were evaluated on individual daily milk weights from 707 half-bred dairy cattle of the Department of Animal Breeding, CCS Haryana Agricultural University, Hisar, India. Both MR and FA used all known test-day yields, while SR used only the last known test-day yield. The SR method was most effective in estimation of yield with minimum average and standard error of absolute bias and distribution of absolute error. Taking the first test on the 15th day for the 15-day test interval and on the 30th day for the 30- and 45-day test intervals resulted in estimation of lactation milk yield with smaller absolute bias and standard error. Part lactation test-day records available up to 210 days were considered to be optimum as there was no significant improvement by utilizing test-day records beyond that. Regular sampling at 45-day intervals with the first test on the 30th day post-partum and subsequent test day records up to 210 days lactation for projecting lactation milk yield by the SR method was recommended as the most practical, simple, and efficient for field recording (7).

The relatively new research topic that has been studied is phenotypic plasticity. This research deals with the ability of individuals or genotype to perform more than one alternative behavior, morphological and physiological forms in response to different environments condition. This research is pioneered by Noor by using *Drosophila buzzatii* as animal model for proving that the phenotypic plasticity phenomena are exist and controlled by genes that can be selected (8). These genes are responsible for the fluctuation of the trait means in different environments. The genetic model of phenotypic plasticity then tested using *Mus musculus* (9, 10, and 11) by using the different protein levels on diet and different salt levels in drinking water. The model is also tested using local ducks (Mojosari and Alabio and their crosses) exposed to different diets containing different aflatoxin levels (12, 13, 14, 15) and PE goat in relation to energy and protein requirements (16). From those experiments it can be concluded that the phenotypic plasticity phenomena are exist in domestic animal. These genes are poly genes and can be selected. It s seems that the genes directly control the genotype by environment interaction. So in the future, we can not

only select our animal for high production, but we can also select the animal that can maintain the high production in different environments.

In order to identify the purity of Bali cattle some molecular biology techniques have been applied including karyotype analysis (17, 18, and 19); scanning electron microscope (18); isoelectric focusing methods (20, 21, 22) and microsatellite (18). The results show that by combining different methods of molecular biology we can get a better result, because each technique has some weaknesses and advantages. In addition, these techniques can be used to identify the purity of Bali cattle and other native species. Some microsatellite loci (HEL 1, INRA035, CSSM66 and INRA037) of Bali cattle have specific band patterns that differ from those of Simmental, Brangus and Limmousin. The A and B alleles at INRA035 microsatellite locus are monomorphic and can be used for specific markers for Bali cattle. Allele A at locus HEL9 that has high frequency (92.90%) in Bali cattle and 100% in Banteng can also be used as a supporting marker (23). The result using scanning electron microscope indicates that Bali cattle hair has specific pattern that different from those of Simmental, Brangus and Limmousin. In the same manner the Isoelectric focusing Methods can differentiate the differences of hemoglobin band patterns among the species.

Considering the facilities and research budget, conventional quantitative genetic techniques still play a major role to improve livestock production in developing countries. However these techniques should be combined with molecular biology techniques such as microsatellite. This technique is needed to get additional information, especially to describe the genetic variation of native animal for conservation.

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